

GCSF-03-2004-B.ST25
SEQUENCE LISTING

<110> Sun, Lee-Hwei K

Sun, Bill

Sun, Cecily R

<120> Fc fusion proteins of human granulocyte colony-stimulating factor with increased biological activities

<130> 03SUN2001-B

<140> to be assigned

<141> 2004-03-15

<150> US 09/968362

<151> 2001-10-01

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

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<210> 2

<211> 27

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<220>

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cggatccggg ctgggcaagg tggcgta 27

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gagcgc当地 gttgtgtcga 20

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ggaattctca tttacccgga gacaggga 28

<210> 5
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<220>

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<400> 5
tggtttctc gatggaggct gggaggcct 29

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<211> 29
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aggcctccca gcctccatcg agaaaacca 29

<210> 7
<211> 69
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<213> Artificial Sequence

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ttgtgtcga 69

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gagtccaaattt atggtcccccc a 21

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 9

ggaattctca tttacccaga gacaggga

28

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 10

cctgagttcg cggggggacc a

21

<210> 11

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

gagtccaaat atggtccccc atgcccacca tgcccagcac ctgagttcgc ggggggacca

60

<210> 12

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12
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tggtccccca 70

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 13
gacaaaactc acacatgccc a 21

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 14
acctgaagtc gcggggggac cgt 23

<210> 15

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 15
gacaaaactc acacatgccc accgtgccc gcacctgaag tcgcggggg accgt 55

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<210> 16
<211> 70
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 16
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cacatgccca 70

<210> 17

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> hG-CSF-L-vFC gamma2 (Figure 2A)

<400> 17
aagcttccca gacccatggc tggacctgcc acccagagcc ccatgaagct gatggccctg 60
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gccagctccc tgccccagag cttcctgctc aagtgcctag agcaagttag gaagatccag 180
ggcgatggcg cagcgctcca ggagaagctg tgtgccacct acaagctgtg ccaccccgag 240
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ctgcagctgg acgtcgccga ctttgcacc accatctggc agcagatgga agaactggga 480
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cgccggcag gaggggtcct agttgcctcc catctgcaga gttccctggg ggtgtcgtac 600
cgcgttctac gccaccttgc ccagcccgaa tccgggtggcg gttccggtgg aggccgaaagc 660
ggcgggtggag gatcagagcg caaatgttgcgt gtcgagtgcc caccgtgccc agcaccac 720
gtggcaggac cgtcagtctt cctttccccc ccaaaaccca aggacaccct catgatctcc 780
cggacccctg aggtcacgtg cgtgggtggtg gacgtgagcc acgaagaccc cgaggtccag 840

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ttcaactgg	acgtggacgg	cgtggagggtg	cataatgcca	agacaaaagcc	acggggaggag	900
cagttcaaca	gcacgttccg	tgtggtcagc	gtcctcaccg	ttgtgcacca	ggactggctg	960
aacggcaagg	agtacaagtg	caaggtctcc	aacaaaggcc	tcccagcctc	catcgagaaa	1020
accatctcca	aaaccaaagg	gcagccccga	gaaccacagg	tgtacaccct	gcccccatcc	1080
cgggaggaga	tgaccaagaa	ccaggtcagc	ctgacctgcc	tggtcaaagg	cttctacccc	1140
agcgacatcg	ccgtggagtg	ggagagcaat	gggcagccgg	agaacaacta	caagaccaca	1200
cctccatgc	tggactccga	cggctccttc	ttcctctaca	gcaagctcac	cgtggacaag	1260
agcaggtggc	agcaggggaa	cgtttctca	tgctccgtga	tgcattgaggc	tctgcacaac	1320
cactacacgc	agaagaccc	ctccctgtct	ccgggtaaat	gagaattc		1368

<210> 18

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> hG-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure 2A)

<400> 18

Met	Ala	Gly	Pro	Ala	Thr	Gln	Ser	Pro	Met	Lys	Leu	Met	Ala	Leu	Gln
1	.	.	5					10				15			

Leu	Leu	Leu	Trp	His	Ser	Ala	Leu	Trp	Thr	Val	Gln	Glu	Ala	Thr	Pro
20							25				30				

Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Cys	Leu
35						40					45				

Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys
50					55					60					

Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu
65					70			75				80			

Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser
						85		90					95		

Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu
100						105				110					

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Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
115 120 125

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
130 135 140

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
145 150 155 160

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
165 170 175

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
180 185 190

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Ser Gly Gly
195 200 205

Gly Ser Gly Gly Ser Gly Gly Gly Ser Glu Arg Lys Cys
210 215 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
290 295 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

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Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 19

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> hG-CSF-L-vFc gamma4 (Figure 2B)

<400> 19
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gccagctccc tgccccagag cttcctgctc aagtgccttag agcaagttag gaagatccag 180
ggcgatggcg cagcgctcca ggagaagctg tgtgccacct acaagctgtg ccaccccgag 240
gagctggtgc tgctcggaca ctctctggc atcccctggg ctccccctgag cagctgcccc 300
agccaggccc tgcagctggc aggctgcttg agccaaactcc atagcggcct tttcctctac 360
caggggctcc tgcaggccct ggaagggttc tcccccgagt tgggtcccac cttggacaca 420
ctgcagctgg acgtcgccga ctttgcacc accatctggc agcagatgg aagaactgg 480
atggcccttg ccctgcagcc cacccagggt gccatgccgg cttcgcctc tgctttccag 540
cgccgggcag gaggggtcct agttgcctcc catctgcaga gcttcctgg ggtgtcgtag 600
cgcgttctac gccaccttgc ccagcccgaa tccggtgccg gttccggtag aggcggaaagc 660
ggcgggtggag gatcagagtc caaatatggt ccccatgcc caccatgccc agcacctgag 720
ttcgcggggg gaccatcagt cttcctgttc ccccaaaac ccaaggacac tctcatgatc 780

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cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 900
gagcagttca acagcacgta ccgtgtggc agcgtcctca ccgtcctgca ccaggactgg 960
ctgaacggca aggagtacaa gtgcaaggc tccaacaaag gcctccgc tcctcatcgag 1020
aaaaccatct ccaaagccaa agggcagccc cgagagccac aggtgtacac cctgccccca 1080
tcccaggagg agatgaccaa gaaccaggc agcctgacct gcctggtcaa aggcttctac 1140
cccagcgaca tcgcccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaggct aaccgtggac 1260
aagagcaggt ggcaggaggg gaatgtctc tcatgctccg tgatgcatga ggctctgcac 1320
aaccactaca cacagaagag cctctccctg tctctggta aatgagaatt c 1371

<210> 20

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2
B)

<400> 20

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln
1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro
20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu
35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
50 55 60

Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu
65 70 75 80

Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
85 90 95

Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
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100	105	110
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu		
115	120	125
Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala		
130	135	140
Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu		
145	150	155
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg		
165	170	175
Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu		
180	185	190
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Ser Gly Gly		
195	200	205
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Ser Lys Tyr		
210	215	220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Ala Gly Gly Pro		
225	230	235
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser		
245	250	255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp		
260	265	270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn		
275	280	285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val		
290	295	300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu		
305	310	315
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys		
325	330	335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr		
340	345	350

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Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
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Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu															
370			375			380									
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu															
385			390			395						400			
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys															
	405			410			415								
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu															
420			425			430									
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly															
435			440			445									

Lys

<210> 21
<211> 1365
<212> DNA
<213> Artificial Sequence

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<223> hG-CSF-L-vFc gamma1 (Figure 2C)

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gccagctccc	tgccccagag	cttcctgctc	aagtgcctag	agcaagtgag	gaagatccag	180
ggcgatggcg	cagcgctcca	ggagaagctg	tgtgccacct	acaagctgtg	ccaccccgag	240
gagctggtgc	tgctcggaca	ctctctggc	atccccctgg	ctccccctgag	cagctgcccc	300
agccaggccc	tgcagctggc	aggctgcttg	agccaaactcc	atagcggcct	tttcctctac	360
caggggctcc	tgcaggccct	ggaagggatc	tcccccgagt	tgggtcccac	cttggacaca	420
ctgcagctgg	acgtcgccga	cttgcacc	accatctggc	agcagatgga	agaactggga	480
atggccctg	ccctgcagcc	cacccaggt	gccatgccgg	cttcgcctc	tgctttccag	540
cgcggggcag	gaggggtcct	agttgcctcc	catctgcaga	gcttcctgga	ggtgtcgtac	600

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cgcgttctac	gccacccgtc	ccagccccga	tccgggtggc	gttccgggtgg	aggcggaa	660
ggcggtggag	gatcagacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagtgcg	720
gggggaccgt	cagtcttcct	cttccccca	aaacccaagg	acaccctcat	gatctccgg	780
acacctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	840
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	900
tacaacagca	cgtaccgggt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	960
ggcaaggagt	acaagtgc当地	ggtctccaac	aaagccctcc	cagcctccat	cgagaaaacc	1020
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatccgg	1080
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	1140
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	1200
cccggtctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	1260
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	1320
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<210> 22

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> hG-CSF-L-vFc gamma1 with a 30-amino acid leader peptide (Figure 2 C)

<400> 22

Met	Ala	Gly	Pro	Ala	Thr	Gln	Ser	Pro	Met	Lys	Leu	Met	Ala	Leu	Gln
1						5			10			15			

Leu	Leu	Leu	Trp	His	Ser	Ala	Leu	Trp	Thr	Val	Gln	Glu	Ala	Thr	Pro
									25			30			

Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Cys	Leu
								35			40		45		

Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys
								50			55		60		

Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu
								65			70		75		80

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Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
85 90 95

Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
100 105 110

Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
115 120 125

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
130 135 140

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
145 150 155 160

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
165 170 175

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
180 185 190

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Ser Gly Gly
195 200 205

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Val Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
325 330 335

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Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 23

<211> 16

<212> PRT

<213> Artificial sequence, 16-amino acid peptide linker

<400> 23

Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 24

<211> 15

<212> PRT

<213> Human IgG1 hinge sequence

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 25

<211> 10

<212> PRT

<213> Truncated human IgG1 hinge sequence

<400> 25

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
1				5					10

<210> 26

<211> 232

<212> PRT

<213> Human IgG1 Fc with native hinge, CH2 and CH3 domains

<400> 26

Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
1				5					10					15	

Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
								25						30	

Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
35						40						45			

Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
50					55					60					

Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70				75					80	

Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
85								90					95		

Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
100							105					110			

Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
115							120					125			

Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
130						135					140				

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Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 27

<211> 228

<212> PRT

<213> Human IgG2 Fc with native hinge, CH2 and CH3 domains

<400> 27

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
100 105 110

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Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Lys
225

<210> 28

<211> 229

<212> PRT

<213> Human IgG4 Fc with native hinge, CH2 and CH3 domains

<400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225